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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2008; month=1; day=23; hr=13; min=45; sec=43; ms=375;]

=====

Reviewer Comments:

<120> A METHOD FOR CREATING A FUNCTIONALLY ACTIVE CHIMERIC TYPE IIG
RESTRICTION ENDONUCLEASE (as amended)

The first line of the above <120> response exceeds the Sequence Rules'
required 72-character line (this includes white spaces). Please insert
a hard return after "TYPE" on the first line, and align the second line.

(from Sequence 2)

Val	Asp	Glu	Ala	Leu	Leu	Ile	Lys	Tyr	His	Gly	Phe	Ser	Glu	Lys	Glu
	515						520					525			

Val	Lys	Gln	Leu	Arg	Gly	Ile	Trp	Lys	Lys	Leu	Ser	Gln	Arg	Arg	Asn
	530						535					540			

Asn	Arg	Thr	Lys	Lys
	545			

Please delete the excess blank lines above: only one blank line should
separate each amino acid line.

<210> 38
<211> 103
<212> PRT
<213> artificial

<220>

<223> segment of protein sequence of catechol O-methyltransferase

<400> 39

Please change the above <210> response to "39." <210> 38 was already shown.

Application No: 10800946

Version No: 2.0

Input Set:

Output Set:

Started: 2008-01-09 14:09:09.990

Finished: 2008-01-09 14:09:12.054

Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 64 ms

Total Warnings: 25

Total Errors: 2

No. of SeqIDs Defined: 43

Actual SeqID Count: 43

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)
W 213	Artificial or Unknown found in <213> in SEQ ID (21)
W 213	Artificial or Unknown found in <213> in SEQ ID (22)
W 213	Artificial or Unknown found in <213> in SEQ ID (23)
W 213	Artificial or Unknown found in <213> in SEQ ID (24)
W 213	Artificial or Unknown found in <213> in SEQ ID (25)
W 213	Artificial or Unknown found in <213> in SEQ ID (26)
W 213	Artificial or Unknown found in <213> in SEQ ID (27)
W 213	Artificial or Unknown found in <213> in SEQ ID (28)
W 213	Artificial or Unknown found in <213> in SEQ ID (29)
W 213	Artificial or Unknown found in <213> in SEQ ID (30)
W 213	Artificial or Unknown found in <213> in SEQ ID (31)
W 213	Artificial or Unknown found in <213> in SEQ ID (32)
W 213	Artificial or Unknown found in <213> in SEQ ID (33)
W 213	Artificial or Unknown found in <213> in SEQ ID (34)
W 213	Artificial or Unknown found in <213> in SEQ ID (35)
W 213	Artificial or Unknown found in <213> in SEQ ID (36)
W 213	Artificial or Unknown found in <213> in SEQ ID (37)
W 213	Artificial or Unknown found in <213> in SEQ ID (38)

Input Set:

Output Set:

Started: 2008-01-09 14:09:09.990
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Error code	Error Description
	This error has occurred more than 20 times, will not be displayed
E 212	Invalid Sequence ID Number; Expected 39 as next SeqID but skipped
E 212	Invalid Sequence ID Number; Expected 39 as next SeqID but skipped

SEQUENCE LISTING

<110> Xu, Shuang-yong
Kobbe, Daniela
Zhu, Zhenyu
Samuelson, James

<120> A METHOD FOR CREATING A FUNCTIONALLY ACTIVE CHIMERIC TYPE IIG RESTRICTION ENDONUCLEASE
(as amended)

<130> NRB-183-CIP

<140> 10800946

<141> 2004-03-15

<150> 10/150,028

<151> 2002-05-17

<150> 09/693,146

<151> 2000-07-02

<160> 43

<170> PatentIn version 3.2 (1-26) and 3.4 (27-43)

<210> 1

<211> 1650

<212> DNA

<213> *Bacillus pumilus*

<220>

<221> CDS

<222> (1)..(1650)

<400> 1

atg aat caa tta att gaa aat gtt aat cta caa aaa tta agg ggt ggg 48
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1 5 10 15

tat tac acc cct aaa gtt att gct gac ttt tta tgt caa tgg agt att 96
Tyr Tyr Thr Pro Lys Val Ile Ala Asp Phe Leu Cys Gln Trp Ser Ile
20 25 30

caa gat gac aca aag agt gta ctt gaa ccc agt tgt gga gat ggt aat 144
Gln Asp Asp Thr Lys Ser Val Leu Glu Pro Ser Cys Gly Asp Gly Asn
35 40 45

ttt att gaa tcg gca ata ctt agg ttc aaa gaa ctt agt ata gat aat 192
Phe Ile Glu Ser Ala Ile Leu Arg Phe Lys Glu Leu Ser Ile Asp Asn
50 55 60

gaa caa ctt aaa gga aga att aca gga gta gag cta att gaa gaa gaa 240
Glu Gln Leu Lys Gly Arg Ile Thr Gly Val Glu Leu Ile Glu Glu Glu
65 70 75 80

gct ttg aaa gtt caa aat cga gca aat gag ttg ggg gtt gat aaa aac 288
Ala Leu Lys Val Gln Asn Arg Ala Asn Glu Leu Gly Val Asp Lys Asn

tca ata gta aat agt gac ttc ttt caa ttt gta aaa gat aat aag aat	336
Ser Ile Val Asn Ser Asp Phe Phe Gln Phe Val Lys Asp Asn Lys Asn	
100 105 110	
aaa aaa ttt gat act att att ggt aat cca cca ttc ata aga tac caa	384
Lys Lys Phe Asp Thr Ile Ile Gly Asn Pro Pro Phe Ile Arg Tyr Gln	
115 120 125	
aac ttt cct gaa gag cat cgt agt ata gcc atg gaa atg atg gag gaa	432
Asn Phe Pro Glu Glu His Arg Ser Ile Ala Met Glu Met Met Glu Glu	
130 135 140	
cta ggt tta aaa cct aat aaa ctt aca aat atc tgg gtt cca ttt cta	480
Leu Gly Leu Lys Pro Asn Lys Leu Thr Asn Ile Trp Val Pro Phe Leu	
145 150 155 160	
gtg gta tct gct aca tta ctt aat gaa caa gga aag atg gct atg gtt	528
Val Val Ser Ala Thr Leu Leu Asn Glu Gln Gly Lys Met Ala Met Val	
165 170 175	
ata cgg gct gaa tta ttt cag gta aag tat gca gca gaa aca aga att	576
Ile Pro Ala Glu Leu Phe Gln Val Lys Tyr Ala Ala Glu Thr Arg Ile	
180 185 190	
ttt tta tca aag ttt ttc gat cgt atc act ata att aca ttt gaa aaa	624
Phe Leu Ser Lys Phe Phe Asp Arg Ile Thr Ile Ile Thr Phe Glu Lys	
195 200 205	
ctt gtt ttt gaa aat atc caa cag gaa gtt ata cta ctt ctt tgt gaa	672
Leu Val Phe Glu Asn Ile Gln Gln Glu Val Ile Leu Leu Leu Cys Glu	
210 215 220	
aag aaa gtt aat aaa ggt aaa gga att cgg gtt att gaa tgc gag aac	720
Lys Lys Val Asn Lys Gly Lys Gly Ile Arg Val Ile Glu Cys Glu Asn	
225 230 235 240	
tta gat gga tta aat tcc att gat ttt gta gct ata aat ggt tca aat	768
Leu Asp Gly Leu Asn Ser Ile Asp Phe Val Ala Ile Asn Gly Ser Asn	
245 250 255	
ggt aaa cct att gaa cac cgt act gaa aag tgg aca aag tat ttc tta	816
Val Lys Pro Ile Glu His Arg Thr Glu Lys Trp Thr Lys Tyr Phe Leu	
260 265 270	
aac gaa gat gaa ata ctt ctt tta cag agt tta aag gaa gac aaa cgc	864
Asn Glu Asp Glu Ile Leu Leu Leu Gln Ser Leu Lys Glu Asp Lys Arg	
275 280 285	
ggt aaa aat tgt aat gac tat ttt aag aca gaa gtt ggc tta gtt act	912
Val Lys Asn Cys Asn Asp Tyr Phe Lys Thr Glu Val Gly Leu Val Thr	
290 295 300	
gga cga aac gaa ttc ttt atg atg aaa gaa aac caa gta aaa gaa tgg	960
Gly Arg Asn Glu Phe Phe Met Met Lys Glu Asn Gln Val Lys Glu Trp	

305	310	315	320	
aat cta gaa gaa tat aca ata cct gtt aca ggt agg tcc aat cag tta				1008
Asn Leu Glu Glu Tyr Thr Ile Pro Val Thr Gly Arg Ser Asn Gln Leu				
325		330	335	
aaa ggt ata aca ttt aca gaa aat gat ttt cat gaa aat tca atg gaa				1056
Lys Gly Ile Thr Phe Thr Glu Asn Asp Phe His Glu Asn Ser Met Glu				
340		345	350	
caa aag gca att cac cta ttt ttg cca cca gat gaa gat ttt gaa aag				1104
Gln Lys Ala Ile His Leu Phe Leu Pro Pro Asp Glu Asp Phe Glu Lys				
355		360	365	
tta ccg att gag tgt caa aat tat atc aag tat ggg gaa gaa aaa ggc				1152
Leu Pro Ile Glu Cys Gln Asn Tyr Ile Lys Tyr Gly Glu Glu Lys Gly				
370		375	380	
ttc cat caa ggc tat aaa acc aga att aga aaa cgt tgg tat ata act				1200
Phe His Gln Gly Tyr Lys Thr Arg Ile Arg Lys Arg Trp Tyr Ile Thr				
385		390	400	
cca tct aga tgg gtt cca gat gct ttt gct tta aga cag gtt gat ggc				1248
Pro Ser Arg Trp Val Pro Asp Ala Phe Ala Leu Arg Gln Val Asp Gly				
405		410	415	
tat cca aaa cta att tta aat gaa acc gac gct tct tct act gat aca				1296
Tyr Pro Lys Leu Ile Leu Asn Glu Thr Asp Ala Ser Thr Asp Thr				
420		425	430	
att cat agg gtt aga ttt aaa gaa ggt ata aat gaa aag tta gcc gta				1344
Ile His Arg Val Arg Phe Lys Glu Gly Ile Asn Glu Lys Leu Ala Val				
435		440	445	
gtt tca ttt ttg aac tca ctc act ttt gca tct tca gaa ata acg ggg				1392
Val Ser Phe Leu Asn Ser Leu Thr Phe Ala Ser Ser Glu Ile Thr Gly				
450		455	460	
aga agt tat ggt ggt ggt gtt atg aca ttc gaa cca act gaa att gga				1440
Arg Ser Tyr Gly Gly Gly Val Met Thr Phe Glu Pro Thr Glu Ile Gly				
465		470	480	
gaa atc cta ata cct tcc ttt gat aac tta tcc att gat ttt gat aaa				1488
Glu Ile Leu Ile Pro Ser Phe Asp Asn Leu Ser Ile Asp Phe Asp Lys				
485		490	495	
att gat gcc tta att cga gaa aag gag att gaa aaa gtc ctt gat att				1536
Ile Asp Ala Leu Ile Arg Glu Lys Glu Ile Glu Lys Val Leu Asp Ile				
500		505	510	
gtt gat gaa gct tta ctt ata aaa tat cat ggg ttt agt gag aaa gaa				1584
Val Asp Glu Ala Leu Leu Ile Lys Tyr His Gly Phe Ser Glu Lys Glu				
515		520	525	
gta aaa cag ctt cga ggg ata tgg aag aaa ctt tct cag aga aga aac				1632
Val Lys Gln Leu Arg Gly Ile Trp Lys Lys Leu Ser Gln Arg Arg Asn				

530

535

540

aat aga acg aag aaa taa

1650

Asn Arg Thr Lys Lys

545

550

<210> 2

<211> 549

<212> PRT

<213> Bacillus pumilus

<400> 2

Met Asn Gln Leu Ile Glu Asn Val Asn Leu Gln Lys Leu Arg Gly Gly

1

5

10

15

Tyr Tyr Thr Pro Lys Val Ile Ala Asp Phe Leu Cys Gln Trp Ser Ile

20

25

30

Gln Asp Asp Thr Lys Ser Val Leu Glu Pro Ser Cys Gly Asp Gly Asn

35

40

45

Phe Ile Glu Ser Ala Ile Leu Arg Phe Lys Glu Leu Ser Ile Asp Asn

50

55

60

Glu Gln Leu Lys Gly Arg Ile Thr Gly Val Glu Leu Ile Glu Glu Glu

65

70

75

80

Ala Leu Lys Val Gln Asn Arg Ala Asn Glu Leu Gly Val Asp Lys Asn

85

90

95

Ser Ile Val Asn Ser Asp Phe Phe Gln Phe Val Lys Asp Asn Lys Asn

100

105

110

Lys Lys Phe Asp Thr Ile Ile Gly Asn Pro Pro Phe Ile Arg Tyr Gln

115

120

125

Asn Phe Pro Glu Glu His Arg Ser Ile Ala Met Glu Met Met Glu Glu

130

135

140

Leu Gly Leu Lys Pro Asn Lys Leu Thr Asn Ile Trp Val Pro Phe Leu

145

150

155

160

Val Val Ser Ala Thr Leu Leu Asn Glu Gln Gly Lys Met Ala Met Val

165

170

175

Ile Pro Ala Glu Leu Phe Gln Val Lys Tyr Ala Ala Glu Thr Arg Ile

180

185

190

Phe Leu Ser Lys Phe Phe Asp Arg Ile Thr Ile Ile Thr Phe Glu Lys

195

200

205

Leu Val Phe Glu Asn Ile Gln Gln Glu Val Ile Leu Leu Leu Cys Glu

210

215

220

Lys Lys Val Asn Lys Gly Lys Gly Ile Arg Val Ile Glu Cys Glu Asn

225	230	235	240
Leu Asp Gly Leu Asn Ser Ile Asp Phe Val Ala Ile Asn Gly Ser Asn			
245	250	255	
Val Lys Pro Ile Glu His Arg Thr Glu Lys Trp Thr Lys Tyr Phe Leu			
260	265	270	
Asn Glu Asp Glu Ile Leu Leu Leu Gln Ser Leu Lys Glu Asp Lys Arg			
275	280	285	
Val Lys Asn Cys Asn Asp Tyr Phe Lys Thr Glu Val Gly Leu Val Thr			
290	295	300	
Gly Arg Asn Glu Phe Phe Met Met Lys Glu Asn Gln Val Lys Glu Trp			
305	310	315	320
Asn Leu Glu Glu Tyr Thr Ile Pro Val Thr Gly Arg Ser Asn Gln Leu			
325	330	335	
Lys Gly Ile Thr Phe Thr Glu Asn Asp Phe His Glu Asn Ser Met Glu			
340	345	350	
Gln Lys Ala Ile His Leu Phe Leu Pro Pro Asp Glu Asp Phe Glu Lys			
355	360	365	
Leu Pro Ile Glu Cys Gln Asn Tyr Ile Lys Tyr Gly Glu Glu Lys Gly			
370	375	380	
Phe His Gln Gly Tyr Lys Thr Arg Ile Arg Lys Arg Trp Tyr Ile Thr			
385	390	395	400
Pro Ser Arg Trp Val Pro Asp Ala Phe Ala Leu Arg Gln Val Asp Gly			
405	410	415	
Tyr Pro Lys Leu Ile Leu Asn Glu Thr Asp Ala Ser Ser Thr Asp Thr			
420	425	430	
Ile His Arg Val Arg Phe Lys Glu Gly Ile Asn Glu Lys Leu Ala Val			
435	440	445	
Val Ser Phe Leu Asn Ser Leu Thr Phe Ala Ser Ser Glu Ile Thr Gly			
450	455	460	
Arg Ser Tyr Gly Gly Gly Val Met Thr Phe Glu Pro Thr Glu Ile Gly			
465	470	475	480
Glu Ile Leu Ile Pro Ser Phe Asp Asn Leu Ser Ile Asp Phe Asp Lys			
485	490	495	
Ile Asp Ala Leu Ile Arg Glu Lys Glu Ile Glu Lys Val Leu Asp Ile			
500	505	510	
Val Asp Glu Ala Leu Leu Ile Lys Tyr His Gly Phe Ser Glu Lys Glu			
515	520	525	

Val Lys Gln Leu Arg Gly Ile Trp Lys Lys Leu Ser Gln Arg Arg Asn
 530 535 540

Asn Arg Thr Lys Lys
 545

<210> 3

<211> 3030

<212> DNA

<213> *Bacillus pumilus*

<220>

<221> CDS

<222> (1)..(3030)

<400> 3

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 1 5 10 15

ttt tta aaa cca act tat aat gaa act caa cta agg aat gat ttt ata 96
 Phe Leu Lys Pro Thr Tyr Asn Glu Thr Gln Leu Arg Asn Asp Phe Ile
 20 25 30

gac cca ctt cta aaa tct tta gga tgg gat gtt gat aat acc aaa gga 144
 Asp Pro Leu Leu Lys Ser Leu Gly Trp Asp Val Asp Asn Thr Lys Gly
 35 40 45

aaa aca cat att cta aga gat gtc att caa gaa gaa tac ata gaa ata 192
 Lys Thr His Ile Leu Arg Asp Val Ile Gln Glu Tyr Ile Glu Ile
 50 55 60

aaa gat gag gag aca aag aaa aat cca gat tat aca ctt cgt ata aac 240
 Lys Asp Glu Glu Thr Lys Lys Asn Pro Asp Tyr Thr Leu Arg Ile Asn
 65 70 75 80

ggc acg aga aag ctg ttt gta gag gtt aag aaa ccg tct ttt aat att 288
 Gly Thr Arg Lys Leu Phe Val Glu Val Lys Lys Pro Ser Phe Asn Ile
 85 90 95

ttg aaa tca gct aaa gca gcc ttc caa aca aga aga tat ggt tgg agt 336
 Leu Lys Ser Ala Lys Ala Ala Phe Gln Thr Arg Arg Tyr Gly Trp Ser
 100 105 110

gct aac ctt ggt att tca gta ctt aca aat ttc gag cat cta gtt att 384
 Ala Asn Leu Gly Ile Ser Val Leu Thr Asn Phe Glu His Leu Val Ile
 115 120 125

tat gat tgt aga tat acg cct gac aaa tcc gac aat gaa cat att gct 432
 Tyr Asp Cys Arg Tyr Thr Pro Asp Lys Ser Asp Asn Glu His Ile Ala
 130 135 140

aga tat aaa gtt ttc tct tac gag gaa tat gaa gaa gca ttt gat gaa 480

Arg	Tyr	Lys	Val	Phe	Ser	Tyr	Glu	Glu	Tyr	Glu	Glu	Ala	Phe	Asp	Glu	
145					150					155					160	
ata	aag	gat	ata	att	tca	tat	gag	tca	gcc	aac	tca	ggt	gct	ctg	gac	528
Ile	Lys	Asp	Ile	Ile	Ser	Tyr	Glu	Ser	Ala	Asn	Ser	Gly	Ala	Leu	Asp	
				165					170					175		
gaa	atg	ttt	gat	gta	aat	aca	aga	gtt	ggf	gaa	acg	ttt	gac	gag	tat	576
Glu	Met	Phe	Asp	Val	Asn	Thr	Arg	Val	Gly	Glu	Thr	Phe	Asp	Glu	Tyr	
			180				185					190				
ttt	tta	cag	caa	att	gag	aat	tgg	cgc	gaa	aag	cta	gct	aaa	act	gca	624
Phe	Leu	Gln	Gln	Ile	Glu	Asn	Trp	Arg	Glu	Lys	Leu	Ala	Lys	Thr	Ala	
			195				200					205				
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Ile	Lys	Asn	Asn	Thr	Glu	Leu	Gly	Glu	Glu	Asp	Val	Asn	Phe	Ile	Val	
	210				215						220					
caa	aga	cta	tta	aac	aga	att	att	ttt	ctt	aga	gtt	tgt	gaa	gat	aga	720
Gln	Arg	Leu	Leu	Asn	Arg	Ile	Ile	Phe	Leu	Arg	Val	Cys	Glu	Asp	Arg	
225				230					235				240			
acc	att	gaa	aaa	tat	gaa	aca	att	aaa	agt	ata	aaa	aac	tat	gag	gaa	768
Thr	Ile	Glu	Lys	Tyr	Glu	Thr	Ile	Lys	Ser	Ile	Lys	Asn	Tyr	Glu	Glu	
				245				250					255			
tta	aaa	gat	ctg	ttt	caa	aag	tct	gat	agg	aaa	ttt	aat	tca	ggt	ctc	816
Leu	Lys	Asp	Leu	Phe	Gln	Lys	Ser	Asp	Arg	Lys	Phe	Asn	Ser	Gly	Leu	
		260					265					270				
ttt	gac	ttc	ata	gat	gat	acg	ctc	ttg	ctt	gag	gtt	gaa	att	gat	tcg	864
Phe	Asp	Phe	Ile	Asp	Asp	Thr	Leu	Leu	Leu	Glu	Val	Glu	Ile	Asp	Ser	
		275				280						285				
aat	gta	ttg	ata	gaa	att	ttt	agt	gat	tta	tat	ttc	cca	caa	agc	cca	912
Asn	Val	Leu	Ile	Glu	Ile	Phe	Ser	Asp	Leu	Tyr	Phe	Pro	Gln	Ser	Pro	
	290				295						300					
tat	gat	ttt	tct	gtt	gtc	gat	cca	aca	ata	tta	agc	cag	ata	tat	gaa	960
Tyr	Asp	Phe	Ser	Val	Val	Asp	Pro	Thr	Ile	Leu	Ser	Gln	Ile	Tyr	Glu	
305				310					315				320			
cgt	ttt	cta	ggt	caa	gaa	ata	att	ata	gag	tca	ggt	ggt	aca	ttt	cac	1008
Arg	Phe	Leu	Gly	Gln	Glu	Ile	Ile	Ile	Glu	Ser	Gly	Gly	Thr	Phe	His	
			325					330					335			
att	acg	gag	tca	cca	gaa	gtt	gcg	gcg	tcc	aat	ggt	gtt	gtt	cca	act	1056
Ile	Thr	Glu	Ser	Pro	Glu	Val	Ala	Ala	Ser	Asn	Gly	Val	Val	Pro	Thr	
			340				345					350				
cca	aaa	att	atc	gtc	gaa	cag	ata	gtg	aaa	gac	act	tta	acg	ccc	ctt	1104
Pro																

370

375

380

ata tgt tgt gga tca gga act ttc cta att tca agt tat gac ttt cta 1200
Ile Cys Cys Gly Ser Gly Thr Phe Leu Ile Ser Ser Tyr Asp Phe Leu
385 390 395 400

gta gag aaa gta atg gaa aag ata ata gaa gag aac atc gat gat tca 12